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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2011; month=5; day=9; hr=12; min=37; sec=34; ms=552;]

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Application No: 08963656 Version No: 2.0

Input Set:

Output Set:

Started: 2011-05-06 10:32:16.872
Finished: 2011-05-06 10:32:19.024
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 152 ms
Total Warnings: 14
Total Errors: 5
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

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SEQUENCE LISTING

<110> GERARD, CRAIG J.
 GERARD, NORMA P.
 MACKAY, CHARLES R.
 PONATH, PAUL D.
 POST, THEODORE W.
 QIN, SHIXIN

<120> ANTIBODIES TO C-C CHEMOKINE RECEPTOR 3 PROTEIN

<130> 079259-0040

<140> 08963656

<141> 1997-11-03

<150> 08/720,565

<151> 1996-09-30

<150> PCT/US96/00608

<151> 1996-01-19

<150> 08/375,199

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<160> 18

<170> PatentIn version 3.5

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<211> 355

<212> PRT

<213> Homo sapiens

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Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Val	Gly	35	40	45	
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His	Asn	Trp	Val	Phe	Gly	His	Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe	100	105	110	
Tyr	His	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu	145	150	155	160
Ala	Val	Leu	Ala	Ala	Leu	Pro	Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu	165	170	175	
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Tyr	Ser	Trp	Arg	His	Phe	His	Thr	Leu	Arg	Met	Thr	Ile	Phe	Cys	Leu	195	200	205	
Val	Leu	Pro	Leu	Leu	Val	Met	Ala	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	210	215	220	
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260 265 270

Cys Glu Arg Thr Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
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Ile Val Phe
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<213> Homo sapiens

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Met Thr Thr Ser Leu Asp Thr
1 5

gtt gag acc ttt ggt acc aca tcc tac tat gat gac gtg ggc ctg ctc 160
Val Glu Thr Phe Gly Thr Thr Ser Tyr Tyr Asp Asp Val Gly Leu Leu
10 15 20

tgt gaa aaa gct gat acc aga gca ctg atg gcc cag ttt gtg ccc ccg 208
Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe Val Pro Pro
25 30 35

ctg tac tcc ctg gtg ttc act gtg ggc ctc ttg ggc aat gtg gtg gtg 256
Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn Val Val Val
40 45 50 55

gtg atg atc ctc ata aaa tac agg agg ctc cga att atg acc aac atc	304
Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met Thr Asn Ile	
60 65 70	
tac ctg ctc aac ctg gcc att tcg gac ctg ctc ttc ctc gtc acc ctt	352
Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Val Thr Leu	
75 80 85	
cca ttc tgg atc cac tat gtc agg ggg cat aac tgg gtt ttt ggc cat	400
Pro Phe Trp Ile His Tyr Val Arg Gly His Asn Trp Val Phe Gly His	
90 95 100	
ggc atg tgt aag ctc ctc tca ggg ttt tat cac aca ggc ttg tac agc	448
Gly Met Cys Lys Leu Leu Ser Gly Phe Tyr His Thr Gly Leu Tyr Ser	
105 110 115	
gag atc ttt ttc ata atc ctg ctg aca atc gac agg tac ctg gcc att	496
Glu Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile	
120 125 130 135	
gtc cat gct gtg ttt gcc ctt cga gcc cgg act gtc act ttt ggt gtc	544
Val His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe Gly Val	
140 145 150	
atc acc agc atc gtc acc tgg ggc ctg gca gtg cta gca gct ctt cct	592
Ile Thr Ser Ile Val Thr Trp Gly Leu Ala Val Leu Ala Ala Leu Pro	
155 160 165	
gaa ttt atc ttc tat gag act gaa gag ttg ttt gaa gag act ctt tgc	640
Glu Phe Ile Phe Tyr Glu Thr Glu Glu Leu Phe Glu Glu Thr Leu Cys	
170 175 180	
agt gct ctt tac cca gag gat aca gta tat agc tgg agg cat ttc cac	688
Ser Ala Leu Tyr Pro Glu Asp Thr Val Tyr Ser Trp Arg His Phe His	
185 190 195	
act ctg aga atg acc atc ttc tgt ctc gtt ctc cct ctg ctc gtt atg	736
Thr Leu Arg Met Thr Ile Phe Cys Leu Val Leu Pro Leu Leu Val Met	
200 205 210 215	
gcc atc tgc tac aca gga atc atc aaa acg ctg ctg agg tgc ccc agt	784
Ala Ile Cys Tyr Thr Gly Ile Ile Lys Thr Leu Leu Arg Cys Pro Ser	
220 225 230	
aaa aaa aag tac aag gcc atc cgg ctc att ttt gtc atc atg gcg gtg	832
Lys Lys Lys Tyr Lys Ala Ile Arg Leu Ile Phe Val Ile Met Ala Val	
235 240 245	
ttt ttc att ttc tgg aca ccc tac aat gtg gct atc ctt ctc tct tcc	880
Phe Phe Ile Phe Trp Thr Pro Tyr Asn Val Ala Ile Leu Leu Ser Ser	
250 255 260	
tat caa tcc atc tta ttt gga aat gac tgt gag cgg agc aag cat ctg	928
Tyr Gln Ser Ile Leu Phe Gly Asn Asp Cys Glu Arg Ser Lys His Leu	
265 270 275	
gac ctg gtc atg ctg gtg aca gag gtg atc gcc tac tcc cac tgc tgc	976

Asp Leu Val Met Leu Val Thr Glu Val Ile Ala Tyr Ser His Cys Cys
280 285 290 295

atg aac ccg gtg atc tac gcc ttt gtt gga gag agg ttc cgg aag tac 1024
Met Asn Pro Val Ile Tyr Ala Phe Val Gly Glu Arg Phe Arg Lys Tyr
300 305 310

ctg cgc cac ttc ttc cac agg cac ttg ctc atg cac ctg ggc aga tac 1072
Leu Arg His Phe Phe His Arg His Leu Leu Met His Leu Gly Arg Tyr
315 320 325

atc cca ttc ctt cct agt gag aag ctg gaa aga acc agc tct gtc tct 1120
Ile Pro Phe Leu Pro Ser Glu Lys Leu Glu Arg Thr Ser Ser Val Ser
330 335 340

cca tcc aca gca gag ccg gaa ctc tct att gtg ttt taggtagatg 1166
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<212> PRT

<213> Homo sapiens

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35 40 45

Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
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120

125

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Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
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Ile Val Phe
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gcttgtagag cgagatcttt ttcataatcc tgctgacaat cgacaggtag ctggccattg	420
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gssatttcca cactctgaga atgacctct tctgtctcgt tctccctctg ctcgttatgg	660
ccatctgcta cacaggaatc atcaaaacgc tgctgaggtg cccagtaaa aaaaagtaca	720
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35 40 45

Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Ph